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tcataatgtt	ccatgaaac	c tctcaagta	c acaattgtat	gttctttgta to	ccttacca	1665
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cgtgggttgg gtcgtacttg ggacctcggc gaagaggacc cgttatttt ttttctttc	180
caaa atg gca gcc tcc agt cgc gca caa gtg tta tct ctg tac cgg gcg Met Ala Ala Ser Ser Arg Ala Gln Val Leu Ser Leu Tyr Arg Ala 1 5 10	229
atg ctg aga gag agc aag cgt ttc agc gcc tac aat tac aga aca tat Met Leu Arg Glu Ser Lys Arg Phe Ser Ala Tyr Asn Tyr Arg Thr Tyr 16 21 26 31	277
gct gtc agg agg ata aga gat gcc ttc aga gaa aat aaa aat gta aag Ala Val Arg Arg Ile Arg Asp Ala Phe Arg Glu Asn Lys Asn Val Lys 32 37 42	325
gat cct gta gaa att caa acc cta gtg aat aaa gcc aag aga gac ctt Asp Pro Val Glu Ile Gln Thr Leu Val Asn Lys Ala Lys Arg Asp Leu 48 53 58 63	373
gga gta att cgt cga cag gtc cac att ggc caa ctg tat tca act gac Gly Val Ile Arg Arg Gln Val His Ile Gly Gln Leu Tyr Ser Thr Asp 64 69 74 79	421
aag ctg atc att gag.aat cga gac atg ccc agg acc tag caagccgggg Lys Leu Ile Ile Glu Asn Arg Asp Met Pro Arg Thr * 80 85 90	470
accagccacc agtggcggcc agggaccacc ttcagcatcc actctctgtt tgagctgggg	530
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<222> (33)..(1835)

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											Ile				ggc Gly 55	197
											Ser				ctg Leu 71	245
															gac Asp 87	293
															ttg Leu 103	341
Leu 104	Glu	Asp	Tyr	Arg	Lys 109	Ile	Ala	Val	Asp	Lys 114	Lys	Gly	Glu	Ala	119	389
Phe 120	Phe	Thr	Ser	Gln	Met 125	atc Ile	Lys	Asp	Cys	Met 130	Lys	Lys	Val	Val	Ala 135	437
Val 136	His	Leu	His	Gln	Thr 141	gtc Val	Gln	Val	Asp	Asp 146	Glu	Leu	Glu	Ile	Lys 151	485
Ala 152	Tyr	Tyr	Ala	Gly	His 157	gtg Val	Leu	Gly	Āla	Ala 162	Met	Phe	Gln	Ile	Lys 167	533
Val 168	Gly	Ser	Glu	Ser	Val 173		Tyr	Thr	Gly	Asp 178	Tyr	Asn	Met	Thr	Pro 183	581
gac Asp 184	Arg	His	Leu	Gly	Ala 189	Ala	Trp	Ile	Asp	Lys 194	Cys	Arg	Pro	Asn	Leu 199	629
ctc Leu 200	Ile	Thr	Glu	Ser	Thr 205	Tyr	Ala	Thr	Thr	Ile 210	Arg	Asp	Ser	Lys	Arg 215	677
tgc Cys 216																725

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	_			_		acc Thr				_	_				gtg Val 263	821
						Gly 999									tac Tyr 279	869
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Gln 376	Val	Leu	Glu	Val	Lys 381	atg Met	Gln	Val	Glu	Tyr 386	Met	Ser	Phe	Ser	Ala 391	1205
His 392	Ala	Asp	Ala	Lys	Gly 397	atc Ile	Met	Gln	Leu	Val 402	Gly	Gln	Ala	Glu	Pro 407	1253
Glu 408	Ser	Val	Leu	Leu	Val 413	cat His	Gly	Glu	Āla	Lys 418	Lys	Met	Glu	Phe	Leu 423	1301
Lys 424	Gln	Lys	Ile	Glu	Gln 429	gag Glu	Leu	Arg	Val	Asn 434	Cys	Tyr	Met	Pro	Ala 439	1349
						ctg Leu			Ser							1397

atc tcg ctg ggg ctg ctg aag cgg gag atg gcg cag ggg ctg ctc cct Ile Ser Leu Gly Leu Leu Lys Arg Glu Met Ala Gln Gly Leu Leu Pro 456 461 466 471	1445
gag gcc aag aag cct cgg ctc ctg cac ggc acc ctg atc atg aag gac Glu Ala Lys Lys Pro Arg Leu Leu His Gly Thr Leu Ile Met Lys Asp 472 487	1493
agc aac ttc cgg ctg gtg tcc tca gag caa gcc ctc aaa gag ctg ggt Ser Asn Phe Arg Leu Val Ser Ser Glu Gln Ala Leu Lys Glu Leu Gly 488 493 498 503	1541
ctg gct gag cac cag ctg cgc ttc acc tgc cgc gtg cac ctg cat gac Leu Ala Glu His Gln Leu Arg Phe Thr Cys Arg Val His Leu His Asp 504 509 514 519	1589
aca cgc aag gag cag gag acg gca ttg cgc gtc tac agc cac ctc aag Thr Arg Lys Glu Gln Glu Thr Ala Leu Arg Val Tyr Ser His Leu Lys 520 525 530 535	1637
agc gtc ctg aag gac cac tgt gtg cag cac ctc cca gac ggc tct gtg Ser Val Leu Lys Asp His Cys Val Gln His Leu Pro Asp Gly Ser Val 536 541 546 551	1685
act gtg gag tcc gtc ctc ctc cag gcc gcc gcc cct tct gag gac cca Thr Val Glu Ser Val Leu Leu Gln Ala Ala Ala Pro Ser Glu Asp Pro 552 557 562 567	1733
ggc acc aag gtg ctg ctg gtc tcc tgg acc tac cag gac gag gag ctg Gly Thr Lys Val Leu Leu Val Ser Trp Thr Tyr Gln Asp Glu Glu Leu 568 573 578 583	1781
ggg agc ttc ctc aca tct ctg ctg aag aag ggc ctc ccc cag gcc ccc Gly Ser Phe Leu Thr Ser Leu Leu Lys Lys Gly Leu Pro Gln Ala Pro 584 589 594 599	1829
agc tga ggccggcaac tcacccagcc gccacctctg ccctctccca gctggacaga Ser * 600	1885
ccctgggcct gcacttcagg actgtgggtg ccctgggtga acagaccctg caggtcccat	1945
ccctggggac agaggccttg tgtcacctgc ctgcccaggc agctgtttgc agctgaagaa	2005
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<213> Homo sapiens

<220>

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tcg cgg ccg cgt cga cca aaa atg gcg gta gtt ggt gtg tcc tcg gtt Ser Arg Pro Arg Arg Pro Lys Met Ala Val Val Gly Val Ser Ser Val 22 27 32 37	150
tct cgg ctg ctg ggt cgg tcc cgc cca cag ctg ggg cgg cct atg tcg Ser Arg Leu Leu Gly Arg Ser Arg Pro Gln Leu Gly Arg Pro Met Ser 38 43 48 53	198
agt ggc gcc cat ggc gaa gag ggc tca gct cgc atg tgg aag act ctc Ser Gly Ala His Gly Glu Glu Gly Ser Ala Arg Met Trp Lys Thr Leu 54 59 64 69	246
acc ttc ttc gtc gcg ctc ccc ggg gtg gca gtc agc atg ctg aat gtg Thr Phe Phe Val Ala Leu Pro Gly Val Ala Val Ser Met Leu Asn Val 70 75 80 85	294
tac ctg aag tcg cac cac gga gag cac gag aga ccc gag ttc atc gcc Tyr Leu Lys Ser His His Gly Glu His Glu Arg Pro Glu Phe Ile Ala 86 91 96 101	342
tac ccc cat ctc cgc atc agg acc aag ccg ttt ccc tgg gga gat ggt Tyr Pro His Leu Arg Ile Arg Thr Lys Pro Phe Pro Trp Gly Asp Gly 102 107 112 117	390
aac cat act cta ttc cat aac cct cat gtg aat cca ctt cca act ggc Asn His Thr Leu Phe His Asn Pro His Val Asn Pro Leu Pro Thr Gly 118 123 128 133	438
tac gaa gat gaa taa agagaatctg gaccactacc cgggcaccag ggaccacagc Tyr Glu Asp Glu * 134	493
actggtttgg accgttactc tgcacatgga ccagaaaaag tatatgggac cttaagctca	553
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<211> 1505

<212> DNA

<213> Homo sapiens

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<222> (72)..(1208)

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tcc Ser 14	ggc Gly	cgt Arg	cgc Arg	cgt Arg	cgc Arg 19	cgc Arg	cgg Arg	ggg ggg	gag Glu	gag Glu 24	ggç ggç	cat His	gat Asp	cca Pro	aag Lys 29	158
_			_	ttg Leu	_		_									206
				agt Ser												254
				gta Val		Arg										302
				act Thr												350
_	_	-		cac His	_	_	_		_	_		-				398
				gag Glu												446
				gtt Val												494
				ttt Phe												542
				cag Gln												590
				gat Asp												638
act	att	aat	999	cat	aat	tgt	gaa	gtg	aaa	aag	gcc	ctt	tct	aaa	caa	686

Th 19	r Ile 0	Asn	Gly	His	Asn 195	Cys	Glu	Val	Lys	Lys 200	Ala	Leu	Ser	Lys	Gln 205	
	g atg u Met 6															734
	t ttt n Phe 2															782
	c cgt y Arg 8															830
	t ggc y Gly 4															878
	t gga e Gly 0															926
	a ggg g Gly 6															974
	a tat y Tyr 2															1022
	ggc Gly															1070
•	tat Tyr				_							-				1118
	ttt Phe															1166
	ggt Gly												taa *	aaac	agc:	1215
aga	aaagg	gc t	acag	ttct	t ag	cagg	agag	aga	gcga	gga	gttg	tcag	ga a	agct	gcagg	1275
tta	cttte	gag a	cagt	cgtc	c ca	aatg	catt	aga	ggaa	ctg	taaa	aatc	tg c	caca	.gaagg	1335
aad	gatga	atc c	atag	tcag	a aa	agtt	actg	cag	ctta	aac	agga	accc	tt c	ttgt	tcagg	1395
act	gtcat	ag c	caca	gttt	g ca	aaag	tgca	gct	attg	att	aatg	catg	ta g	tgtc	aatta	1455
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gaaaccccag gcgtggagat tgatcctgcg agagaagggg gttcatc atg gcg gat
                                                                       176
                                                      Met Ala Asp
                                                         1
gac cta aag cga ttc ttg tat aaa aag tta cca agt gtt gaa ggg ctc
                                                                       224
Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu
  4
cat gcc att gtt gtg tca gat aga gat gga gta cct gtt att aaa gtg
                                                                       272
His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val Ile Lys Val
                     25
                                          30
gca aat gac aat gct cca gag cat gct ttg cga cct ggt ttc tta tcc
                                                                       320
Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly Phe Leu Ser
                     41
                                          46
act ttt gcc ctt gca aca gac caa gga agc aaa ctt gga ctt tcc aaa
                                                                       368
Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys
 52
                     57
                                          62
aat aaa agt atc atc tgt tac tat aac acc tac cag gtg gtt caa ttt
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Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe
 68
                     73
                                          78
aat cgt tta cct ttg gtg gtg agt ttc ata gcc agc agc agt gcc aat
                                                                      464
Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn
 84
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aca gga cta att gtc agc cta gaa aag gaa ctt gct cca ttg ttt gaa
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Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu
100
                    105
                                         110
                                                             115
gaa ctg aga caa gtt gtg gaa gtt tct taa t ctgacagtgg tttcagtgtg
                                                                      563
Glu Leu Arg Gln Val Val Glu Val Ser
116
                    121
taccttatct tcattataac aacacaatat caatccagca atctttagac tacaataata
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cttttatcca tgtgctcaag aaagggcccc tttttccaac ttatactaaa gagctagcat
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<213> Homo sapiens

<220>
<221> CDS

<400> 546

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Met Ala Ser Ala Gly Gly
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gaa gac tgc gag agc ccc gcg ccg gag gcc gac cgt ccg cac cag cgg
Glu Asp Cys Glu Ser Pro Ala Pro Glu Ala Asp Arg Pro His Gln Arg
7 12 17 22

ccc ttc ctg ata ggg gtg agc ggc act gcc agc ggg aag tcg acc
Pro Phe Leu Ile Gly Val Ser Gly Gly Thr Ala Ser Gly Lys Ser Thr
23 28 33

gtg tgt gag aag atc atg gag ttg ctg gga cag aac gag gtg gaa cag 256 Val Cys Glú Lys Ile Met Glu Leu Gly Gln Asn Glu Val Glu Gln 39 44 49 54

	_		_		_	Ile	_	_	_	_	Arg			_	gtc Val 70	304
-	_	_		_	_	gcc Ala	_	-	_		Gly	_				352
_			-	_		gat Asp		_	_	_				_	_	400
						acg Thr										448
						gag Glu										496
						ttg Leu										544
						ttc Phe										592
						gac Asp										640
						acc Thr										688
_	_	_		_	_	tat Tyr	_	-								736
						aac Asn										784
_			_		_	aaa Lys			_							832
_		_				tct Ser				_				_	_	880
						cat His	_			_	_	_			tga * 278	928
9999	ctgo	cg a	gcct	cago	ıg ca	iggto	tece	gcc	cggc	atg	tgtg	ttca	.gg a	actg	agcct	988

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tg	tctggg	tt q	gcct	9 9 99	tg a	tcct	ccct	c ct	gcgt	ggtg	gct	gtct	ctg	gaaa	gcatcc	1108
ct	tgccgc	tg (ccac	gggc	ag c	ccca	gccc	c cg	tccg	tcca	ggo	tcac	cca	cagt	agtgat	1168
gc	agacgt	ga (cgtg	gggg	aa g	19999	ctga	g cc	ctgt	ggct	999	ttct	gac	aact	gtaacg	1228
gt	tttgtc	ga g	gctt	aggc	cc c	tttg	gagg	g ag	aatc	aata	aat	aaca	aac	acca	actaaa	1288
		0>	547 2670								B					
	<21	2 > I	ANC	can	ienc											
			101110	sap	rens											
		1> (2>	(107)) (634)											
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Th	a att o r Ile (163
	a gat o g Asp I 0															211
	c aac a u Asn I 6															259
	a ctt a u Leu A 2															307
	a atc o y Ile (8															355
	a gaa t s Glu I 4														Leu 99	403
	a atg a e Met S					Glu										451

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aag gaa ctg caa gca cat gtt gac cag ata act gaa atg gca gca gta Lys Glu Leu Gln Ala His Val Asp Gln Ile Thr Glu Met Ala Ala Val 132 137 142 147	547
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tcaaataact cgagaatcat ttttgaacct aaggaaagat gatgcgtcgg aaagtacttc	704
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<211> 1764

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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agtgagtgat ggattggaac tgagaccgaa atataatgga attttacatt gcttgactac 180
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agcc atg acc ctc tgc att aca aac cca tta tgg gta aca aaa act cgc 409
Met Thr Leu Cys Ile Thr Asn Pro Leu Trp Val Thr Lys Thr Arg

ctt atg tta cag tat gat gct gtt gtt aac tcc cca cac cga caa tat Leu Met Leu Gln Tyr Asp Ala Val Val Asn Ser Pro His Arg Gln Tyr 16 21 26 31	457
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cgt gga tta tat aag gga ttt gtt cct ggg ctg ttt gga aca tcg cat Arg Gly Leu Tyr Lys Gly Phe Val Pro Gly Leu Phe Gly Thr Ser His 48 53 58 63	553
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391

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							_				Glu				cag Gln 146	487
		_								_	Asp				999 Gly 162	535
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Phe Leu Glu Asn Met Glu Val Glu Cys Asn Tyr His Cys Tyr His Glu
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                                          26
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Lys Asp Pro Asp Gly Cys Tyr Arg Leu Val Asp Tyr Leu Glu Gly Ile
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Arg Lys Asn Phe Asp Glu Ala Ala Lys Val Leu Lys Phe Asn Cys Glu
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                                          74
                                                               79
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Thr Gly Lys Gly Gly Leu Thr Gln Asp Leu Lys Ala Ala Ala Arg Cys
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Phe Leu Met Ala Cys Glu Lys Pro Gly Lys Lys Ser Ile Ala Ala Cys
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His Asn Val Gly Leu Leu Ala His Asp Gly Gln Val Asn Glu Asp Gly
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Gln Pro Asp Leu Gly Lys Ala Arg Asp Tyr Tyr Thr Arg Ala Cys Asp
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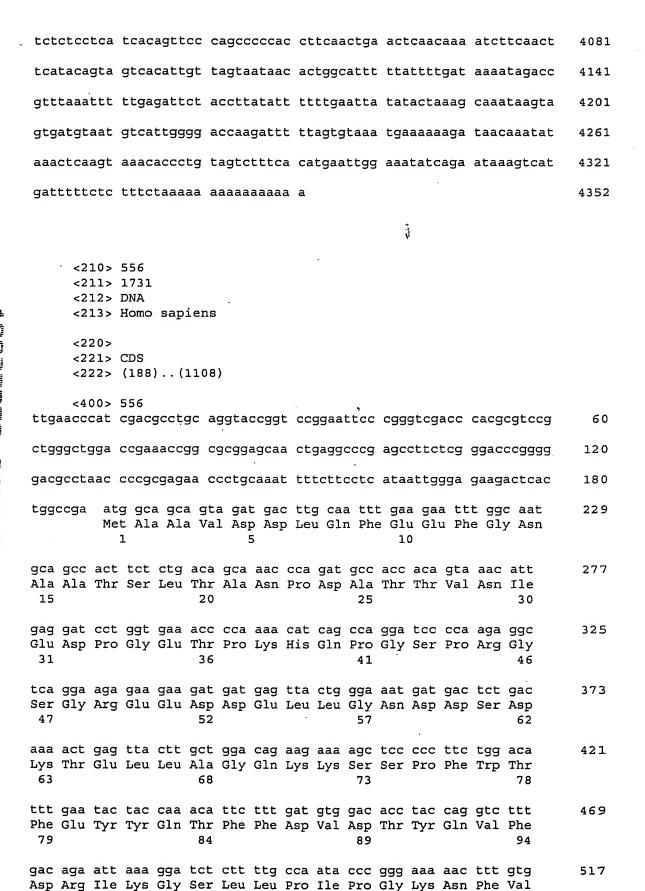
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aaa ttg tct gag aaa	acc cag caa gca	gtg agg ggg gat gag	tct ttc 1121
Lys Leu Ser Glu Lys	Thr Gln Gln Ala	Val Arg Gly Asp Glu	Ser Phe
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	Ala		ttc Phe													1937
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Asn 614	Val	·Val	ttc Phe	Thr	Ser 619	His	Thr	Thr	Glu	Gln 624	Arg	His	Pro	Leu	Leu 629	2225
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                         Met Asp His Lys Ser Pro Gly Asn Lys Gly
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Ser Leu Val Tyr Ala Gly Ile Lys Ser Ile Val Lys Ser Ser Leu Gly
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Gly Trp Ile Lys Lys Gly Thr Asp Val Asp Val Gly Pro Phe Leu Asn
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tcc ctt gta caa gaa ggg gaa tgg gaa aga gct gct gct gtg gca ttg
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Ser Leu Val Gln Glu Gly Glu Trp Glu Arg Ala Ala Val Ala Leu
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Phe Asn Leu Asp Ile Arg Arg Ala Ile Gln Ile Leu Asn Glu Gly Ala
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Ser Ser Glu Lys Gly Asp Leu Asn Leu Asn Val Val Ala Met Ala Leu
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107
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Ser Gly Tyr Thr Asp Glu Lys Asn Ser Leu Trp Arg Glu Met Cys Ser
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123
aca ctg cga tta cag cta aat aac ccg tat ttg/tgt gtc atg ttt gca
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Thr Leu Arg Leu Gln Leu Asn Asn Pro Tyr Leu Cys Val Met Phe Ala
139
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ga G1 20	g gct u Ala 3	gga Gly	aat Asn	ttg Leu	gaa Glu 208	gga Gly	att Ile	ttg Leu	ctt Leu	aca Thr 213	gg¢ Gly	ctt Leu	act Thr	aaa Lys	gat Asp 218	735
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Ser Arg Ser Ala	Lys Lys Cys		lu Lys Ala Glu L	ys Ala
77	82		87	. 92
aaa att aaa aag	gcc att cag	Lys Gly Asn M	tg gaa gtt gcg a	gg ata 337
Lys Ile Lys Lys	Ala Ile Gln :		et Glu Val Ala A	rg Ile
93	98		03	108
cac gcc gaa aat	gcc atc cgc	Gln Lys Asn G	ag gcg gtg aat t	tc ttg 385
His Ala Glu Asn	Ala Ile Arg		ln Ala Val Asn P	he Leu
109	114		19	124
aga atg agt gcg Arg Met Ser Ala 125	cga gtc gat (Arg Val Asp 1	Ala Val Ala A	cc agg gtc cag a la Arg Val Gln T 35	cg gcg 433 hr Ala 140
		Lys Ser Met A	ct ggt gtg gtt a la Gly Val Val L 51	
atg gat gcg aca	ttg aag acc a	Met Asn Leu G	ag aag att tot g	ct ttg · 529
Met Asp Ala Thr	Leu Lys Thr 1		lu Lys Ile Ser A	la Leu
157	162		67	172
		Phe Glu Thr Le	tg gac gtc cag a eu Asp Val Gln T 83	
caa atg gaa gac	acg atg agc a	Ser Thr Thr T	cg ctc acc act co	cc cag 625
Gln Met Glu Asp	Thr Met Ser s		hr Leu Thr Thr P:	ro Gln
189	194		99	204
aac caa gtg gat	atg ctg ctc of	Gln Glu Met A	ca gat gag gcg g	gc ctc 673
Asn Gln Val Asp	Met Leu Leu 0		la Asp Glu Ala G	ly Leu
205	210		15	220
gac ctc aac atg	gag ctg_ccg (cag ggc cag a	cc ggc tcc gtg g	gc acg 721

Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val Gly Thr 221 226 231 236	
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acg cac cca agc ctc cgc ctc cgc gcg act cgg cgg cat tac tag tga Met Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile 12 17 22 27	639
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tac tag tga att cac tag taa tgt cgc gcg gag gcg gag gct tgg gtg Lys Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro 44 49 54 59	735
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		Thr			_	_		_				Asn		_		agt Ser 26	160
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L		Pro				aaa Lys 48											256
4. diffic other bank		Leu				act Thr 64											304
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		Thr				ata Ile 96											400
						gct Ala 112											448
						aaa Lys 128											496
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Ile Lys Pro Asn Gln	caa gac att agt Gln Asp Ile Ser 608	ttt gtc agt ttt act Phe Val Ser Phe Thr 613	tgt gtt 1936 Cys Val 618
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		gag Glu														2464
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		gtg Val														2752

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				cat His 1					Arg					Arg		3328
				cag Gln 1					Val					Phe		3376
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					Asn		Glu			Leu		His			Ile	gaa Glu 1178	3616
					Glu		.aaa Lys			Ser					Ser	caa Gln 1194	3664
					Glu		ttt Phe			Ser					His		3712
That dies fant dies then they that					Ser		ggc Gly			Glu					Lys		3760
Amb ibi dad					Ile		gtt Val			Leu					Lys		3808
Trees that II II II II					Leu		gat Asp			Asp					Leu		3856
					Asn		cag Gln			Thr					Gln		3904
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5033

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                                                    atq qct qqa
                                                    Met Ala Gly
342
Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Gly Leu Leu Val Ala
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Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val Pro Arg Thr
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                                                                    534
Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro Ala Val Tyr
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•							ttc Phe										1206
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												ccc Pro				1446
												aca Thr			tct Ser 403	1494
												aag Lys				1542
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gcg Ala 436																1638
gcc Ala 452																1686
ccc Pro 468									Lys							1734
ctc Leu 484				Ser		9999	ga c	cagg	cago	c ct	cago	agcc	aca	ıggcc	ttc	1788
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						ggc Gly										960
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gaa	cca	ggc	cca	aca	gcc	cca	tac	ctg	ggc	cga	tcg	atg	tct	tac	agc	1152

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		t Se 1	r Gl	n Gl		s Gl [.] 5	u Ası	n Gl	u Hi	s Phe		g As:	p Ly	s Se	r Glu	
~++									•			44-				205
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							ata Ile									492
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					tac Tyr 453			_							_	1692
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					gáa Glu 501											1836
					tac Tyr 517											1884
					agt Ser 533											1932
					aaa Lys 549											1980 /
	aaa Lys		tga *	tga	gtat	atgo	tt a	tgtt	ctca	ıt aa	atga	aggt	ctc	ıttta	ıgaa	2035

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	101					106					111					116	
	_	_				-					_	Leu				cca Pro 132	498
	_	_				_			_			Pro			_	cct Pro 148	546
																aag Lys 164	594
												aag Lys				gtc Val 180	642
												ctg Leu				gag Glu 196	690
												ttc Phe					738
												atc Ile					786
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		-			_	_		_				cta Leu		_			882
												aat Asn					930
												gag Glu					978
	_		_	-					-			att Ile	_	_	_		1026
į	_			_	_	_	_				_	tca Ser		_			1074
•				aaa Lys		taa * 330	agac	at a	cact	gaaa	it tt	taag	ıttgg	ggt	gtta	aaa	1128

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						gac Asp										721
	_					ttc Phe			_						_	769
						gac Asp										817
						ggt Gly										865
						cgc Arg										913
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							cga Arg						624

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			c gcc tgc cta gcg r Ala Cys Leu Ala 315	
		a Ser Ile Le	g att cac gga aca u Ile His Gly Thr 331	
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			g gcc ctg att gaa u Ala Leu Ile Glu 363	
			g cgc tgt gca cag n Arg Cys Ala Gln 379	
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			g ttt ccc tgt tct n Phe Pro Cys Ser 411	
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						gaa Glu										786
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Val Gly Arg Phe Ile Met Gly Ile Asp Gly Gly Val Ala Leu Ser Val
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		_			atg Met 231	_			_	_				_		1015
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Ala Ala Ala Ser Leu Ser Arg Ala Ala Ala Glu Cys Leu Leu Ala Arg
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Gly Pro Gly Val Arg Ala Ala Pro Pro Arg Asp Pro Arg Pro Ser His
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Pro Glu Pro Arg Gly Cys Gly Ala Ala Pro Gly Arg Thr Leu His Phe

acc gcg gct gtc ccc gcc ggg cac aac aag tgg tcc aaa gtc agg cac
Thr Ala Ala Val Pro Ala Gly His Asn Lys Trp Ser Lys Val Arg His
53 68 68

47

42

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Ile Lys Gly Pro Lys Asp Val Glu Arg Ser Arg Ile Phe Ser Lys Leu
69 74 79 84

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Cys Leu Asn Ile Arg Leu Ala Val Lys Glu Gly Gly Pro Asn Pro Glu

85 90 95 100

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His Asn Ser Asn Léu Ala Asn Ile Leu Glu Val Cys Arg Ser Lys His
101 106 111 116

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Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro Pro Lys Lys Asp
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Lys Leu Gln Thr Lys Arg Lys Lys Pro Arg Arg Tyr Trp Glu Glu Glu
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Thr Val Pro Thr Thr Ala Gly Ala Ser Pro Gly Pro Pro Arg Asn Lys
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Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn Ala Tyr Ile Leu
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aag aag tot ogg ato tot aag aag oot oag gto oog aag aaa ooc oga
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Lys Lys Ser Arg Ile Ser Lys Lys Pro Gln Val Pro Lys Lys Pro Arg
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gaa tgg aag aac ccg gag tcc cag cgc ggc ttg tcc ggg gcc caa gat
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81
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Pro Phe Pro Gly Pro Ala Pro Val Pro Val Glu Val Val Gln Lys Phe
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                                                             112
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Cys Arg Ile Asp Lys Ser Arg Lys Leu Pro His Ser Lys Ala Lys Thr
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_						tta Leu				_	_	-	_			1176
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577 58	82	587	592
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aag aat cgg gag ctc cg Lys Asn Arg Glu Leu Ar 49	gt cct cag aga cca a rg Pro Gln Arg Pro 1 54	aaa aat gct tac atc Lys Asn Ala Tyr Ile 59	tta 312 Leu 64
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acc gta gac gag tac aaa att gga cag ctg tac atg atc agc aaa cac Thr Val Asp Glu Tyr Lys Ile Gly Gln Leu Tyr Met Ile Ser Lys His 13 28 28	579

					cgg Arg							aat Asn 44	627
					cac His							aag Lys 60	675
					aaa Lys								723
					aca Thr								771
			_		tgt Cys		_	_					819
	-		_		gac Asp			_		_			867
					gtg Val								915
					gag Glu								963
_			_		aag Lys				_	_			1011
	_	_	_	_	cct Pro	_	_			-	_		1059
					gly ggg								1107
					att Ile								1155
					tat Tyr								1203
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gct gcc cgg att ttg atg tgc cat tgc ctg gca gcc att gcc atg caa Ala Ala Arg Ile Leu Met Cys His Cys Leu Ala Ala Ile Ala Met Gln 29 34 39 44	267
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							Ala				Arg				cat His 124	507
							Tyr				Thr	Gln			tca Ser 140	555
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dien frem fram fram fant		_		gct Ala	_									_	tcc Ser 188	699
Her Start			_	gct Ala	-			_			_		_	_	_	747
Sud B Burt				ctc Leu												795
-tig				aat Asn												843
				atg Met												891
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				gat Asp												987
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Ala 413	Leu	Lys	Val	Glu	Gly 418	gtg Val	Val	Gln	His	Gly 423	Ser	Lys	Pro	Gly	Leu 428	1419
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	_				_	gaa Glu				_			_			1563
Phe 477	Leu	Leu	Asn	Phe	Ala 482	atc Ile	Leu	Gly	Thr	His 487	Asn	Ile	Thr	Val	Glu 492	1611
Ser 493	Ser	Val	Lys	Asp	Ala 498	Asn	Gly	Ile	Val	Trp 503	Lys	Thr	Gly	Pro	Arg 508	1659
Thr 509	Thr	Ile	Phe	Val	Lys 514	tcc Ser	Leu	Glu	Asp	Pro 519	Tyr	Ser	Gln	Gln	Ile 524	1707
cgc			~~~		~~~	~~~	~~~	000	~~~	t t a	CaG	CaG	Cad	cac	C22	1755

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atcoctogaa tocaccagca ogagogtooc accogogoot gggaco atg goo act Met Ala Thr 1	175
gac tca tgg gcc ctg gcg gtg gac gag cag gaa gct gcg gct gag tcg Asp Ser Trp Ala Leu Ala Val Asp Glu Gln Glu Ala Ala Ala Glu Ser 4 9 14 19	223
ttg agc aac ttg cat ctt aag gaa gag aaa atc aaa cca gat acc aat Leu Ser Asn Leu His Leu Lys Glu Glu Lys Ile Lys Pro Asp Thr Asn 20 25 30 35	271
ggt gct gtt gtc aag acc aat gcc aat gca gag aag aca gat gaa gaa Gly Ala Val Val Lys Thr Asn Ala Asn Ala Glu Lys Thr Asp Glu Glu 36 41 46 51	319
gag aaa gag gac aga gct gcc cag tcc tta ctc aac aag ctg atc aga Glu Lys Glu Asp Arg Ala Ala Gln Ser Leu Leu Asn Lys Leu Ile Arg	367

					gat Asp												415
	cca Pro 84	aac Asn	tcc Ser	cct Pro	ctg Leu	tac Tyr 89	tcg Ser	gtg Val	aag Lys	tct Ser	ttt Phe 94	gaa Glu	gag Glu	ctt Leu	cgg Arg	ctg Leu 99	463
	aaa Lys 100	cca Pro	cag Gln	ctt Leu	ctc Leu	caa Gln 105	gga Gly	gtc Val	tat Tyr	gcc Ala	atg Met 110	ggt Gly	ttc Phe	aat Asn	cgt Arg	cca Pro 115	511
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L	cag Gln 132	aac Asn	tta Leu	att Ile	gcc Ala	caa Gln 137	tct Ser	cag Gln	tct Ser	ggt Gly	act Thr 142	ggt Gly	aaa Lys	aca Thr	gct Ala	gcc Ala 147	607
the state of the state of	ttc Phe 148	gtg Val	ctg Leu	gcc Ala	atg Met	ctt Leu 153	agc Ser	caa Gln	gta Val	gaa Glu	cct Pro 158	gca Ala	aac Asn	aaa Lys	tac Tyr	ccc Pro 163	655
That Ben Sen	cag Gln 164	tgt Cys	cta Leu	tgt Cys	ctc Leu	tcc Ser 169	cca Pro	acg Thr	tat Tyr	gag Glu	c,tc Leu 174	gcc Ala	ctc Leu	caa Gln	aca Thr	gga Gly 179	703
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					ggc Gly												799
					ggc Gly												847
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1					tct Ser												1039
	cca	aac	gtt	atc	aaa	ctg	aag	cgt	gag	gaa	gag	acc	ctg	gac	acc	atc	1087

Pro 292	Asn	Val	Ile	ГÀг	Leu 297	Lys	Arg	Glu	Glu ·	Glu 302	Thr	Leu	Asp	Thr	Ile 307	
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							atc Ile									1183
							agt Ser									1231
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							gtg Val									1519
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284

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atc cag aag aag cta cag gga gaa gtg gag aaa tat caa cag cta cag Ile Gln Lys Lys Leu Gln Gly Glu Val Glu Lys Tyr Gln Gln Leu Gln 332 aaq gac tta agt aaa tcc atg tcg ggg agg cag aaa ctt gaa gca caa Lys Asp Leu Ser Lys Ser Met Ser Gly Arg Gln Lys Leu Glu Ala Gln 21 26 380 cta aca qaa aat aat atc gtg aaa gag gaa ctg gcc ctg ctg gat ggg Leu Thr Glu Asn Asn Ile Val Lys Glu Glu Leu Ala Leu Leu Asp Gly 37 42 47 tcc aac gtg gtc ttt aaa ctt ctg ggt ccg gtg cta gtc aaa cag gag 428 Ser Asn Val Val Phe Lys Leu Leu Gly Pro Val Leu Val Lys Gln Glu 53 58

476 ctg ggg gag gct cgg gcc aca gta ggg aag agg ctg gac tat atc aca Leu Gly Glu Ala Arg Ala Thr Val Gly Lys Arg Leu Asp Tyr Ile Thr 69 79 74 gct gaa att aag cga tac gaa tcc cag ctt cgg gat ctt gag cgg cag 524 Ala Glu Ile Lys Arg Tyr Glu Ser Gln Leu Arg Asp Leu Glu Arg Gln 85 95 90

572 tca gag caa cag agg gag acc ctt gct cag ctg cag çag gag ttc cag Ser Glu Gln Gln Arg Glu Thr Leu Ala Gln Leu Gln Gln Glu Phe Gln 101 106 111

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acccagcgcc c	ettgtetege ac	ccagtagg ct	ttcatccc	cgcc atg gcg ga Met Ala Gl 1	g ctg 236 u Leu
				tat caa cag cta Tyr Gln Gln Leu	
				aaa ctt gaa gca Lys Leu Glu Ala	
				gac tgg gat ttg Asp Trp Asp Leu	
				atc aca tat gtc Ile Thr Tyr Val	
				tcc aac gtg gtc Ser Asn Val Val	
				ctg ggg gag gct Leu Gly Glu Ala	

85 90 95 100	
gcc aca gta ggg aag agg ctg gac tat atc aca gct gaa att aag cga Ala Thr Val Gly Lys Arg Leu Asp Tyr Ile Thr Ala Glu Ile Lys Arg 101 106 111 116	572
tac gaa tcc cag ctt cgg gat ctt gag cgg cag tca gag caa cag agg Tyr Glu Ser Gln Leu Arg Asp Leu Glu Arg Gln Ser Glu Gln Gln Arg 117 122 127 132	620
gag acc ctt gct cag ctg cag cag gag ttc cag cgg gcc cag gca gca Glu Thr Leu Ala Gln Leu Gln Gln Glu Phe Gln Arg Ala Gln Ala Ala 133 138 143	668
aag gca ggg gct cct ggc aag gcc tga cccca tggtgggggg aggggagggg	720
aggggaggga atgaggcagc tctaggatct atactgtagc taataaaatg taaaaacacc	780
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ctttcaattt gggcacagac cctgtttctt taagaaatta tccctataaa atatgtgact	30,0
catgtgaa atg aat ttg aaa aat att tcg ggc tta att att agt aaa aag Met Asn Leu Lys Asn Ile Ser Gly Leu Ile Ile Ser Lys Lys 1 5 10	350
aac tgt tcc aga aag aag cct gat gag ttt aat gta tgt gag aaa ttg Asn Cys Ser Arg Lys Lys Pro Asp Glu Phe Asn Val Cys Glu Lys Leu	398

		Leu					Glu					Gly				tat Tyr 46	446
		Tyr										His				agt Ser 62	494
																ggc Gly 78	542
																gga Gly 94	590
÷					aaa Lys												638
का भेगम प्रमा फार्स		_	_		ata Ile			_			_	_	_		_		686
and the same than					tgc Cys												734
					ctt Leu												782
					tgt Cys												830
					att Ile												878
					ctc Leu												926
			_		aat Asn	_			_			_	_	_			974
			_		cgg Arg	-	-				_				_	-	1022
					aaa Lys												1 ₁ 070
	cag	aga	aca	cac	aca	gga	gag	aag	ccc	tat	gaa	tgt	act	gaa	tgt	999	1118

Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly 255 260 265 270	
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gtg aag tca aac ctc act gaa cat cag aga aca cac aca ggg gag aag Val Lys Ser Asn Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys 303 308 313 318	1262
ccc tat gaa tgt aat gca tgt ggg aaa tcc ttc tgc cac aga tca gcc Pro Tyr Glu Cys Asn Ala Cys Gly Lys Ser Phe Cys His Arg Ser Ala 319 324 329 334	1310
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caa aga act cac act ggg gag aaa cca tat aag tgt aat gaa tgt ggg Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly 367 372 377 382	1454
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Met Ala Leu Arg Glu Leu Lys Val Cys Leu Leu Gly Asp Thr

1 5 10

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Gly Val Gly Lys Ser Ser Ile Val Trp Arg Phe Val Glu Asp Ser Phe
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Asp Pro Asn Ile Asn Pro Thr Ile Gly Ala Ser Phe Met Thr Lys Thr
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Val Gln Tyr Gln Asn Glu Leu His Lys Phe Leu Ile Trp Asp Thr Ala
47 52 57 62

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736

gaa atc gct cga ctt cta atg gct gaa gaa.aag aaa gct tac aaa aaa

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														aaa Lys		832
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atat	tggc	ca c	ctct	atgo	et go	atat	actt	ctt	ggga	atat	agta	tcta	ag a	acctt	tgtaa	1270
acto	gccat	tt t	gtta	aggta	at gg	gagtt	tggt	ato	ctago	ggag	tagg	cctt	at t	tago	caattc	1330
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gaat	ataa	iga a	atag	gcttt	t to	ıttgo	atta	ato	gtato	gata	tttt	gaag	ıga o	cagag	geettt	1450
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												gag Glu 20		161
												cta Leu 36		209
												gag Glu 52		257
												gcc Ala 68		305
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					cta Leu									401
	_	_	_		gct Ala	_	 		_	_		aac Asn 116		449
					ctg Leu									497
					cag Gln									545
					cag Gln									593
					acc Thr									641
		_		_	ccc Pro	_		_	_					689
					ggt Gly							cgg Arg 212		737
					atc Ile									785

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		 _			gat Asp	_	_	_			-	881
-					aat Asn							929
					cgg Arg							977
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					aac Asn							1025
dina tum dina tyan tumb tumb					gag Glu							1073
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					acg Thr							1121
					tgc Cys							1169
					gca Ala							1217
					gcc Ala							1265
					tat Tyr							1313
					gta Val							1361
					cat His							1409
					Gly Gly							1457

	tac Tyr 453	aag Lys	gcc Ala	tgc Cys	aaa Lys	gtg Val 458	agc Ser	agc Ser	ccc Pro	aca Thr	gtg Val 463	aac Asn	act Thr	act Thr	ctg Leu	aga Arg 468	1505
						tat Tyr 474											1553
		_		_	_	gcc Ala 490	_										1601
						gca Ala 506											1649
						cac His 522											1697
Aine thus Aine Lane Sud Tech						agg Arg 538											1745
And dan 4						ctt Leu 554											1793
hadi His Shall Se that						cag Gln 570											1841
thus thus	gag Glu 581	tag *	ctag	jetet	ga g	gccc	caag	g t <u>s</u>	ıggta	ıcaaa	ı gca	ıggta	tgg	ccct	caga	ıga	1897
	tgca	gcct	gc t	gctg	gctt	t to	agto	agag	ggt	tggg	ggc	tggc	cago	ca a	gctg	ccttg	1957
	ccct	ggcc	gc t	ctta	ctcc	c to	ecto	tgct	gto	tcac	ttc	aggt	ccat	gt a	tttc	acttt	2017
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(3 35	gagac	cta	ccat	agaa	gt t	cgaa	gatg	t ag	Me	-					t gaa s Glu	174
	Thr								_		_				agc Ser 23	222
	Leu														gta Val 39	270
	tca Ser				-	_	-				-					318
	agt Ser		_						_			_	_		_	366
	gct Ala	_	_				_			-					_	414
_	gac Asp	_								_	_	_				462
_	aat Asn					-		_	_	_					_	510
	aga Arg	_			-							_		-		558
	ctt Leu															606
	gat Asp															654
	cag Gln															702
	agc Ser															750
	tca Ser															798

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											gaa Glu					1230
											ata Ile					1278
											cat His					1326
act Thr 392	caa Gln	cca Pro	gaa Glu	atg Met	cat His 397	aaa Lys	tat Tyr	ggt Gly	cag Gln	tta Leu 402	gtt Val	aaa Lys	gta Val	gaa Glu	tta Leu 407	1374
Glu 408	Glu	Asn	Ala	Glu	Asp 413	Asp	Lys	Thr	Glu	Asn 418	caa Gln /	Ile	Pro	Gln	Arg 423	1422
atg Met 424	act Thr	aga Arg	aac Asn	aaa Lys	gca Ala 429	aat Asn	aca Thr	atg Met	gca Ala	aat Asn 434	caa Gln	agc Ser	aaa Lys	cag Gln	att Ile 439	1470

	_	_	-					_		_	agt Ser	_			1518
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											cag Gln				1614
											cag ⁱ Gln				1662
-		_	_					-			cag Gln				1710
	_	_					_		_		ata Ile				1758
_	_		_			_	-	_			cct Pro		-		1806
		-	-		_						tat Tyr				1854
				-		_					aca Thr				1902
		_							_		cag Gln				1950
											gaa Glu				1998
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141

136